

5 What is claimed is:

1. A method of determining the genotype at a locus within genetic material obtained from a biological sample, the method comprising:

10 A. reacting the material at the locus to produce a first reaction value indicative of the presence of a given allele at the locus;

 B. forming a data set including the first reaction value;

15 C. establishing a distribution set of probability distributions, including at least one distribution, associating hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

20 D. applying the first reaction value to each pertinent probability distribution to determine a measure of the conditional probability of each genotype of interest at the locus; and

25 E. determining the genotype based on the data obtained from step (D).

30 2. A method according to claim 1, wherein the distribution set includes a plurality of probability distributions for a corresponding plurality of genotypes of interest.

 3. A method, according to claim 1, further comprising:

5 (i) reacting the material at the locus to produce a second reaction value independently indicative of the presence of a second allele at the locus;

(ii) forming a second data set including the second reaction value; and

10 (iii) applying the first and second reaction values to each pertinent distribution to determine a measure of the conditional probability of each genotype at the locus.

15 4. A method according to claim 2, further comprising:

(i) reacting the material at the locus to produce a second reaction value;

20 (ii) applying the first and second reaction values to each pertinent distribution to determine the probability of each genotype at the locus; and

(iii) applying the first and second reaction values to each pertinent distribution to determine a measure of the conditional probability of each genotype at the locus.

25 5. A method according to claim 3, wherein each probability distribution associates a hypothetical pair of first and second reaction values with a single probability of each genotype of interest.

30 6. A method according to claim 4, wherein each probability distribution associates a hypothetical pair of

5 first and second reaction values with a single probability
of each genotype of interest.

10 7. A method according to claim 1, wherein:
step (B) includes the step of including in the
data set other reaction values obtained under conditions
comparable to those under which the first reaction value was
produced; and

15 step (C) includes the step of using the reaction
values in the data set to establish the probability
distributions; the method further comprising:

performing steps (D) and (E) with respect to each
of the reaction values.

20 8. A method according to claim 2, wherein:
step (B) includes the step of including in the
data set other reaction values obtained under conditions
comparable to those under which the first reaction value was
produced; and

25 step (C) includes the step of using the reaction
values in the data set to establish the probability
distributions; the method further comprising:

performing steps (D) and (E) with respect to each
of the reaction values.

30 9. A method according to claim 3, wherein:
step (B) includes the step of including in the
data set other reaction values obtained under conditions

5 comparable to those under which the first reaction value was produced; and

step (C) includes the step of using the reaction values in the data set to establish the probability distributions; the method further comprising:

10 performing steps (D) and (E) with respect to each of the reaction values in the first and second data sets.

10. A method according to claim 4, wherein:

15 step (B) includes the step of including in the data set other reaction values obtained under conditions comparable to those under which the first reaction value was produced; and

20 step (C) includes the step of using the reaction values in the data set to establish the probability distributions; the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values in the first and second data sets.

25 11. A method, according to claim 7, of determining the genotype at a locus within genetic material obtained from each of a plurality of samples, the method further comprising:

(1) performing step (A) with respect to the locus of material obtained from each sample;

30 (2) in step (B), including in the data set reaction values obtained from each sample.

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5 12. A method according to claim 7, of determining the genotype of selected loci within genetic material obtained from a sample, the method further comprising:

(1) performing step (A) at each of the selected loci;

10 (2) in step (B), including in the data set reaction values obtained from each of the selected loci.

13. A method according to claim 7, wherein step (C) includes:

5 (1) establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

20 (2) using the initial probability distributions to determine measures of the initial conditional probability for each genotype at the locus; and

25 (3) using the results of step (2) to modify the initial probability distributions, so that the modified distributions more accurately reflect the reaction values in the data set.

14. A method according to claim 8, wherein step (C) includes:

30 (1) establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

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5 (2) using the initial probability distributions to determine measures of the initial conditional probability for each genotype at the locus; and

(3) using the results of step (2) to modify the initial probability distributions, so that the modified
10 distributions more accurately reflect the reaction values in the data set.

15 15. A method according to claim 9, wherein step (C) includes:

(1) establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

(2) using the initial probability distributions to determine measures of the initial conditional probability for each genotype at the locus; and
20

(3) using the results of step (2) to modify the initial probability distributions, so that the modified distributions more accurately reflect the reaction values in
25 the data set.

16. A method according to claim 10, wherein step (C) includes:

(1) establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;
30

5 (2) using the initial probability distributions to determine initial conditional probabilities for each genotype at the locus; and

(3) using the results of step (2) to modify the initial probability distributions, so that the modified
10 distributions more accurately reflect the reaction values in the data.

17. A method according to claim 13, wherein step (C) further includes:

15 (4) repeating steps (1) through (3) a desired number of times.

18. A method according to claim 14, wherein step (C) further includes:

20 (4) repeating steps (1) through (3) a desired number of times.

19. A method according to claim 15, wherein step (C) further includes:

25 (4) repeating steps (1) through (3) a desired number of times.

20. A method according to claim 16, wherein step (C) further includes:

30 (4) repeating steps (1) through (3) a desired number of times.

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26. A method according to claim 4, wherein each allele is a single nucleotide.

27. A method according to claim 1, wherein each allele consists of at least two specific nucleotides.

28. A method according to claim 4, wherein each allele consists of at least two specific nucleotides.

29. A method according to claim 1, wherein each allele is defined at least in part by its length in nucleotides.

30. A method according to claim 4, wherein each allele is defined at least in part by its length in nucleotides.

31. A method according to claim 1, wherein each allele is defined by one of the presence and absence of at least one restriction site.

32. A method according to claim 4, wherein each allele is defined by one of the presence and absence of at least one restriction site.

33. A method according to claim 4, wherein step (E) includes the step of including in the data set reaction values from prior tests at the locus obtained under

5 comparable conditions.

34. A method according to claim 12, wherein the loci are selected on the basis of their ability to discriminate among subjects.

10 35. A method, according to claim 3, wherein the step A of reacting the material involves using a different reaction from that of step A and the second allele is different from the given allele.

15 36. A method according to claim 1, wherein step (A) includes the step of assaying for the given allele using genetic bit analysis.

20 37. A method according to claim 1, wherein step (A) includes the step of assaying for the given allele using hybridization.

25 38. A method, according to claim 1, wherein step (A) includes the step of assaying for the given allele using allele-specific amplification.

30 39. A method, according to claim 1, wherein step (A) includes the step of assaying for the given allele using a polymerase chain reaction.

40. A method, according to claim 1, wherein step

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5 (A) includes the step of assaying for the given allele using
a ligase chain reaction.

10 41. A method according to claim 12, wherein the
loci are proximal to one another, so that the set of
genotypes so produced may indicate a sequence of nucleotides
associated with the genetic material.

15 42. A method of determining the genotype of a
subject, the method comprising:

20 A. reacting genetic material taken from the
subject at selected loci, each locus being an identified
single nucleotide, to produce with respect to each of the
selected loci a reaction value indicative of the presence of
a given allele at each of the selected loci;

25 B. using the reaction values to determine the
genotype of the subject and a confidence score, associated
with the genotype being determined.

30 43. A method according to claim 42, wherein the
loci are selected to provide information pertaining to
inheritance of a trait.

44. A method according to claim 42, wherein the
loci are selected to provide information pertaining to
parentage of the subject.

45. A method according to claim 42, wherein the

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5 loci are selected to provide information pertaining to the
identity of the subject.

10 46. A method according to claim 42, wherein the
loci are selected to provide information pertaining to
matching tissue of the subject with that of a donor.

15 47. A method according to claim 42, wherein the
loci are spaced throughout the entire genome of the subject
to assist in characterizing the genome of the species of the
subject.

add
B1

ADD
C4

ADD
D1

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